

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/573,508
Source: IFWP
Date Processed by STIC: 04/06/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/06/2006

PATENT APPLICATION: US/10/573,508

TIME: 10:35:09

Input Set : A:\002.00280sequenclisting.txt

Output Set: N:\CRF4\04062006\J573508.raw

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3 <110> APPLICANT: Kimber, Wendy
4   Alessi, Dario
6 <120> TITLE OF INVENTION: Methods
8 <130> FILE REFERENCE: 002.00280
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/573,508
C--> 10 <141> CURRENT FILING DATE: 2006-03-27
10 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/004060
11 <151> PRIOR FILING DATE: 2004-09-27
13 <150> PRIOR APPLICATION NUMBER: GB 0322689.1
14 <151> PRIOR FILING DATE: 2003-09-27
16 <160> NUMBER OF SEQ ID NOS: 33
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 11
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial
25 <220> FEATURE:
26 <223> OTHER INFORMATION: PTP signature motif of phosphatase domain
28 <220> FEATURE:
29 <221> NAME/KEY: MISC_FEATURE
30 <222> LOCATION: (1)..(1)
31 <223> OTHER INFORMATION: V or I
34 <220> FEATURE:
35 <221> NAME/KEY: MISC_FEATURE
36 <222> LOCATION: (7)..(7)
37 <223> OTHER INFORMATION: any amino acid
40 <220> FEATURE:
41 <221> NAME/KEY: MISC_FEATURE
42 <222> LOCATION: (10)..(10)
43 <223> OTHER INFORMATION: any amino acid
46 <400> SEQUENCE: 1
W--> 48 Xaa His Cys Ser Ala Gly Xaa Gly Arg Xaa Gly
49 1          5          10
52 <210> SEQ ID NO: 2
53 <211> LENGTH: 2485
54 <212> TYPE: PRT
55 <213> ORGANISM: Homo sapiens
57 <400> SEQUENCE: 2
59 Met His Val Ser Leu Ala Glu Ala Leu Glu Val Arg Gly Gly Pro Leu
60 1          5          10          15
63 Gln Glu Glu Glu Ile Trp Ala Val Leu Asn Gln Ser Ala Glu Ser Leu
64          20          25          30
67 Gln Glu Leu Phe Arg Lys Val Ser Leu Ala Asp Pro Ala Ala Leu Gly

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68          35          40          45
71 Phe Ile Ile Ser Pro Trp Ser Leu Leu Leu Leu Pro Ser Gly Ser Val
72      50          55          60
75 Ser Phe Thr Asp Glu Asn Ile Ser Asn Gln Asp Leu Arg Ala Phe Thr
76 65          70          75          80
79 Ala Pro Glu Val Leu Gln Asn Gln Ser Leu Thr Ser Leu Ser Asp Val
80          85          90          95
83 Glu Lys Ile His Ile Tyr Ser Leu Gly Met Thr Leu Tyr Trp Gly Ala
84          100          105          110
87 Asp Tyr Glu Val Pro Gln Ser Gln Pro Ile Lys Leu Gly Asp His Leu
88          115          120          125
91 Asn Ser Ile Leu Leu Gly Met Cys Glu Asp Val Ile Tyr Ala Arg Val
92          130          135          140
95 Ser Val Arg Thr Val Leu Asp Ala Cys Ser Ala His Ile Arg Asn Ser
96 145          150          155          160
99 Asn Cys Ala Pro Ser Phe Ser Tyr Val Lys His Leu Val Lys Leu Val
100          165          170          175
103 Leu Gly Asn Leu Ser Gly Thr Asp Gln Leu Ser Cys Asn Ser Glu Gln
104          180          185          190
107 Lys Pro Asp Arg Ser Gln Ala Ile Arg Asp Arg Leu Arg Gly Lys Gly
108          195          200          205
111 Leu Pro Thr Gly Arg Ser Ser Thr Ser Asp Val Leu Asp Ile Gln Lys
112          210          215          220
115 Pro Pro Leu Ser His Gln Thr Phe Leu Asn Lys Gly Leu Ser Lys Ser
116 225          230          235          240
119 Met Gly Phe Leu Ser Ile Lys Asp Thr Gln Asp Glu Asn Tyr Phe Lys
120          245          250          255
123 Asp Ile Leu Ser Asp Asn Ser Gly Arg Glu Asp Ser Glu Asn Thr Phe
124          260          265          270
127 Ser Pro Tyr Gln Phe Lys Thr Ser Gly Pro Glu Lys Lys Pro Ile Pro
128          275          280          285
131 Gly Ile Asp Val Leu Ser Lys Lys Lys Ile Trp Ala Ser Ser Met Asp
132          290          295          300
135 Leu Leu Cys Thr Ala Asp Arg Asp Phe Ser Ser Gly Glu Thr Ala Thr
136 305          310          315          320
139 Tyr Arg Arg Cys His Pro Glu Ala Val Thr Val Arg Thr Ser Thr Thr
140          325          330          335
143 Pro Arg Lys Lys Glu Ala Arg Tyr Ser Asp Gly Ser Ile Ala Leu Asp
144          340          345          350
147 Ile Phe Gly Pro Gln Lys Met Asp Pro Ile Tyr His Thr Arg Glu Leu
148          355          360          365
151 Pro Thr Ser Ser Ala Ile Ser Ser Ala Leu Asp Arg Ile Arg Glu Arg
152          370          375          380
155 Gln Lys Lys Leu Gln Val Leu Arg Glu Ala Met Asn Val Glu Glu Pro
156 385          390          395          400
159 Val Arg Arg Tyr Lys Thr Tyr His Gly Asp Val Phe Ser Thr Ser Ser
160          405          410          415
163 Glu Ser Pro Ser Ile Ile Ser Ser Glu Ser Asp Phe Arg Gln Val Arg
164          420          425          430

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167 Arg Ser Glu Ala Ser Lys Arg Phe Glu Ser Ser Ser Gly Leu Pro Gly
168      435      440      445
171 Val Asp Glu Thr Leu Ser Gln Gly Gln Ser Gln Arg Pro Ser Arg Gln
172      450      455      460
175 Tyr Glu Thr Pro Phe Glu Gly Asn Leu Ile Asn Gln Glu Ile Met Leu
176 465      470      475      480
179 Lys Arg Gln Glu Glu Glu Leu Met Gln Leu Gln Ala Lys Met Ala Leu
180      485      490      495
183 Arg Gln Ser Arg Leu Ser Leu Tyr Pro Gly Asp Thr Ile Lys Ala Ser
184      500      505      510
187 Met Leu Asp Ile Thr Arg Asp Pro Leu Arg Glu Ile Ala Leu Glu Thr
188      515      520      525
191 Ala Met Thr Gln Arg Lys Leu Arg Asn Phe Phe Gly Pro Glu Phe Val
192      530      535      540
195 Lys Met Thr Ile Glu Pro Phe Ile Ser Leu Asp Leu Pro Arg Ser Ile
196 545      550      555      560
199 Leu Thr Lys Lys Gly Lys Asn Glu Asp Asn Arg Arg Lys Val Asn Ile
200      565      570      575
203 Met Leu Leu Asn Gly Gln Arg Leu Glu Leu Thr Cys Asp Thr Lys Thr
204      580      585      590
207 Ile Cys Lys Asp Val Phe Asp Met Val Val Ala His Ile Gly Leu Val
208      595      600      605
211 Glu His His Leu Phe Ala Leu Ala Thr Leu Lys Asp Asn Glu Tyr Phe
212      610      615      620
215 Phe Val Asp Pro Asp Leu Lys Leu Thr Lys Val Ala Pro Glu Gly Trp
216 625      630      635      640
219 Lys Glu Glu Pro Lys Lys Lys Thr Lys Ala Thr Val Asn Phe Thr Leu
220      645      650      655
223 Phe Phe Arg Ile Lys Phe Phe Met Asp Asp Val Ser Leu Ile Gln His
224      660      665      670
227 Thr Leu Thr Cys His Gln Tyr Tyr Leu Gln Leu Arg Lys Asp Ile Leu
228      675      680      685
231 Glu Glu Arg Met His Cys Asp Asp Glu Thr Ser Leu Leu Leu Ala Ser
232      690      695      700
235 Leu Ala Leu Gln Ala Glu Tyr Gly Asp Tyr Gln Pro Glu Val His Gly
236 705      710      715      720
239 Val Ser Tyr Phe Arg Met Glu His Tyr Leu Pro Ala Arg Val Met Glu
240      725      730      735
243 Lys Leu Asp Leu Ser Tyr Ile Lys Glu Glu Leu Pro Lys Leu His Asn
244      740      745      750
247 Thr Tyr Val Gly Ala Ser Glu Lys Glu Thr Glu Leu Glu Phe Leu Lys
248      755      760      765
251 Val Cys Gln Arg Leu Thr Glu Tyr Gly Val His Phe His Arg Val His
252      770      775      780
255 Pro Glu Lys Lys Ser Gln Thr Gly Ile Leu Leu Gly Val Cys Ser Lys
256 785      790      795      800
259 Gly Val Leu Val Phe Glu Val His Asn Gly Val Arg Thr Leu Val Leu
260      805      810      815
263 Arg Phe Pro Trp Arg Glu Thr Lys Lys Ile Ser Phe Ser Lys Lys Lys

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```

264      820      825      830
267 Ile Thr Leu Gln Asn Thr Ser Asp Gly Ile Lys His Gly Phe Gln Thr
268      835      840      845
271 Asp Asn Ser Lys Ile Cys Gln Tyr Leu Leu His Leu Cys Ser Tyr Gln
272      850      855      860
275 His Lys Phe Gln Leu Gln Met Arg Ala Arg Gln Ser Asn Gln Asp Ala
276 865      870      875      880
279 Gln Asp Ile Glu Arg Ala Ser Phe Arg Ser Leu Asn Leu Gln Ala Glu
280      885      890      895
283 Ser Val Arg Gly Phe Asn Met Gly Arg Ala Ile Ser Thr Gly Ser Leu
284      900      905      910
287 Ala Ser Ser Thr Leu Asn Lys Leu Ala Val Arg Pro Leu Ser Val Gln
288      915      920      925
291 Ala Glu Ile Leu Lys Arg Leu Ser Cys Ser Glu Leu Ser Leu Tyr Gln
292      930      935      940
295 Pro Leu Gln Asn Ser Ser Lys Glu Lys Asn Asp Lys Ala Ser Trp Glu
296 945      950      955      960
299 Glu Lys Pro Arg Glu Met Ser Lys Ser Tyr His Asp Leu Ser Gln Ala
300      965      970      975
303 Ser Leu Tyr Pro His Arg Lys Asn Val Ile Val Asn Met Glu Pro Pro
304      980      985      990
307 Pro Gln Thr Val Ala Glu Leu Val Gly Lys Pro Ser His Gln Met Ser
308      995      1000      1005
311 Arg Ser Asp Ala Glu Ser Leu Ala Gly Val Thr Lys Leu Asn Asn
312      1010      1015      1020
315 Ser Lys Ser Val Ala Ser Leu Asn Arg Ser Pro Glu Arg Arg Lys
316      1025      1030      1035
319 His Glu Ser Asp Ser Ser Ser Ile Glu Asp Pro Gly Gln Ala Tyr
320      1040      1045      1050
323 Val Leu Gly Met Thr Met His Ser Ser Gly Asn Ser Ser Ser Gln
324      1055      1060      1065
327 Val Pro Leu Lys Glu Asn Asp Val Leu His Lys Arg Trp Ser Ile
328      1070      1075      1080
331 Val Ser Ser Pro Glu Arg Glu Ile Thr Leu Val Asn Leu Lys Lys
332      1085      1090      1095
335 Asp Ala Lys Tyr Gly Leu Gly Phe Gln Ile Ile Gly Gly Glu Lys
336      1100      1105      1110
339 Met Gly Arg Leu Asp Leu Gly Ile Phe Ile Ser Ser Val Ala Pro
340      1115      1120      1125
343 Gly Gly Pro Ala Asp Leu Asp Gly Cys Leu Lys Pro Gly Asp Arg
344      1130      1135      1140
347 Leu Ile Ser Val Asn Ser Val Ser Leu Glu Gly Val Ser His His
348      1145      1150      1155
351 Ala Ala Ile Glu Ile Leu Gln Asn Ala Pro Glu Asp Val Thr Leu
352      1160      1165      1170
355 Val Ile Ser Gln Pro Lys Glu Lys Ile Ser Lys Val Pro Ser Thr
356      1175      1180      1185
359 Pro Val His Leu Thr Asn Glu Met Lys Asn Tyr Met Lys Lys Ser
360      1190      1195      1200

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```

363 Ser Tyr Met Gln Asp Ser Ala Ile Asp Ser Ser Ser Lys Asp His
364      1205      1210      1215
367 His Trp Ser Arg Gly Thr Leu Arg His Ile Ser Glu Asn Ser Phe
368      1220      1225      1230
371 Gly Pro Ser Gly Gly Leu Arg Glu Gly Ser Leu Ser Ser Gln Asp
372      1235      1240      1245
375 Ser Arg Thr Glu Ser Ala Ser Leu Ser Gln Ser Gln Val Asn Gly
376      1250      1255      1260
379 Phe Phe Ala Ser His Leu Gly Asp Gln Thr Trp Gln Glu Ser Gln
380      1265      1270      1275
383 His Gly Ser Pro Ser Pro Ser Val Ile Ser Lys Ala Thr Glu Lys
384      1280      1285      1290
387 Glu Thr Phe Thr Asp Ser Asn Gln Ser Lys Thr Lys Lys Pro Gly
388      1295      1300      1305
391 Ile Ser Asp Val Thr Asp Tyr Ser Asp Arg Gly Asp Ser Asp Met
392      1310      1315      1320
395 Asp Glu Ala Thr Tyr Ser Ser Ser Gln Asp His Gln Thr Pro Lys
396      1325      1330      1335
399 Gln Glu Ser Ser Ser Ser Val Asn Thr Ser Asn Lys Met Asn Phe
400      1340      1345      1350
403 Lys Thr Phe Ser Ser Ser Pro Pro Lys Pro Gly Asp Ile Phe Glu
404      1355      1360      1365
407 Val Glu Leu Ala Lys Asn Asp Asn Ser Leu Gly Ile Ser Val Thr
408      1370      1375      1380
411 Gly Gly Val Asn Thr Ser Val Arg His Gly Gly Ile Tyr Val Lys
412      1385      1390      1395
415 Ala Val Ile Pro Gln Gly Ala Ala Glu Ser Asp Gly Arg Ile His
416      1400      1405      1410
419 Lys Gly Asp Arg Val Leu Ala Val Asn Gly Val Ser Leu Glu Gly
420      1415      1420      1425
423 Ala Thr His Lys Gln Ala Val Glu Thr Leu Arg Asn Thr Gly Gln
424      1430      1435      1440
427 Val Val His Leu Leu Leu Glu Lys Gly Gln Ser Pro Thr Ser Lys
428      1445      1450      1455
431 Glu His Val Pro Val Thr Pro Gln Cys Thr Leu Ser Asp Gln Asn
432      1460      1465      1470
435 Ala Gln Gly Gln Gly Pro Glu Lys Val Lys Lys Thr Thr Gln Val
436      1475      1480      1485
439 Lys Asp Tyr Ser Phe Val Thr Glu Glu Asn Thr Phe Glu Val Lys
440      1490      1495      1500
443 Leu Phe Lys Asn Ser Ser Gly Leu Gly Phe Ser Phe Ser Arg Glu
444      1505      1510      1515
447 Asp Asn Leu Ile Pro Glu Gln Ile Asn Ala Ser Ile Val Arg Val
448      1520      1525      1530
451 Lys Lys Leu Phe Pro Gly Gln Pro Ala Ala Glu Ser Gly Lys Ile
452      1535      1540      1545
455 Asp Val Gly Asp Val Ile Leu Lys Val Asn Gly Ala Ser Leu Lys
456      1550      1555      1560
459 Gly Leu Ser Gln Gln Glu Val Ile Ser Ala Leu Arg Gly Thr Ala

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/06/2006
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,7,10
Seq#:27; N Pos. 594
Seq#:31; N Pos. 6,12,15
Seq#:32; N Pos. 2,10,14,19

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,30,31,32,33

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:4623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:540
L:4697 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:4733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0